SEQUENCE LISTING

<110> University of Utah Research Foundation
Bock, Susan C.
Hobden, Adrian N.

<120> VARIANTS OF ANTITHROMBIN III

<130> 21101.0021P1

<150> 60/384,599
<151> 2002-05-31

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Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
20 25 30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35 40 45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50 55 60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65 70 75 80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
85 90 95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
100 105 110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
115 120 125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
130 135 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145 150 155 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
165 170 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr

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Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
        195                 200                 205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
    210                 215                 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                 230                 235                 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                245                 250                 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
            260                 265                 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
        275                 280                 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
    290                 295                 300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                 310                 315                 320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325                 330                 335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
            340                 345                 350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
        355                 360                 365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
    370                 375                 380
Ala Leu Glu Ala Asn Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                 390                 395                 400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
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Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
20 25 30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35 40 45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50 55 60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65 70 75 80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr

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Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
            100                 105                 110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
        115                 120                 125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
    130                 135                 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145                 150                 155                 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
                165                 170                 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
            180                 185                 190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
        195                 200                 205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
    210                 215                 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                 230                 235                 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                245                 250                 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
            260                 265                 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
        275                 280                 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
    290                 295                 300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                 310                 315                 320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325                 330                 335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
            340                 345                 350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
        355                 360                 365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
    370                 375                 380
Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                 390                 395                 400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                405                 410                 415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420                 425                 430

<210> 78
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 78
Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
 1               5                  10                  15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
            20                  25                  30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
        35                  40                  45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
    50                  55                  60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
```

65 70 75 80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
85 90 95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
100 105 110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
115 120 125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
130 135 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145 150 155 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
165 170 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
180 185 190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
195 200 205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
210 215 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225 230 235 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
245 250 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
260 265 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
275 280 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
290 295 300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305 310 315 320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
325 330 335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
340 345 350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
355 360 365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
370 375 380
Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385 390 395 400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
405 410 415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
420 425 430

<210> 79
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 79
agccctgtgg acatctgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt 60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag 120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc 180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt 240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg 300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc 360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca 420

```
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt     480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc     540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt     600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag     660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct     720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc     780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc     840
ctcatcttgc ccaagcctga gaagagcctg gccaaggtgg agaaggaact caccccagag     900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tggtggtcca catgccccgc     960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat    1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc    1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg    1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc    1200
aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc    1260
atgggcagag tagccaaccc ttgtgttaag taa                                 1293

<210> 80
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 80
agtcccgtag atatatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt      60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag     120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc     180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt     240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg     300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc     360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca     420
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt     480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc     540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt     600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag     660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct     720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc     780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc     840
ctcatcttgc ccaagcctga gaagagcctg gccaaggtgg agaaggaact caccccagag     900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tggtggtcca catgccccgc     960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat    1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc    1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg    1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc    1200
aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc    1260
atgggcagag tagccaaccc ttgtgttaag taa                                 1293

<210> 81
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 81
Ser Pro Val Asp Val Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
 1               5                  10                  15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
            20                  25                  30
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Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
        35                  40                  45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
    50                  55                  60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65                  70                  75                  80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
                85                  90                  95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
            100                 105                 110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
        115                 120                 125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
    130                 135                 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145                 150                 155                 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
                165                 170                 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
            180                 185                 190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
        195                 200                 205

Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
    210                 215                 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                 230                 235                 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                245                 250                 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
            260                 265                 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
        275                 280                 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
    290                 295                 300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                 310                 315                 320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325                 330                 335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
            340                 345                 350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
        355                 360                 365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
    370                 375                 380
Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                 390                 395                 400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                405                 410                 415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420                 425                 430

<210> 82
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 82
agccctgtgg acgtatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt      60
```

taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag 120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc 180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt 240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg 300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc 360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca 420
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt 480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc 540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt 600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag 660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct 720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc 780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc 840
ctcatcttgc ccaagcctga gaagagcctg gccaaggtgg agaaggaact caccccagag 900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tggtggtcca catgccccgc 960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat 1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc 1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg 1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc 1200
aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc 1260
atgggcagag tagccaaccc ttgtgttaag taa 1293

<210> 83
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 83
agtcccgtag atgtgtgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt 60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag 120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc 180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt 240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg 300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc 360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca 420
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt 480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc 540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt 600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag 660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct 720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc 780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc 840
ctcatcttgc ccaagcctga gaagagcctg gccaaggtgg agaaggaact caccccagag 900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tggtggtcca catgccccgc 960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat 1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc 1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg 1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc 1200
aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc 1260
atgggcagag tagccaaccc ttgtgttaag taa 1293

<210> 84
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 84
Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1 5 10 15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
20 25 30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35 40 45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50 55 60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65 70 75 80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
85 90 95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
100 105 110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
115 120 125

Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
130 135 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145 150 155 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
165 170 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
180 185 190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
195 200 205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
210 215 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225 230 235 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
245 250 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
260 265 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
275 280 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
290 295 300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305 310 315 320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
325 330 335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
340 345 350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
355 360 365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
370 375 380
Ala Leu Glu Ala Tyr Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385 390 395 400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
405 410 415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
420 425 430

<210> 85
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 85

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His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1               5                  10                  15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
            20                  25                  30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
        35                  40                  45
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
    50                  55                  60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
65                  70                  75                  80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
                85                  90                  95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
            100                 105                 110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
        115                 120                 125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
    130                 135                 140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145                 150                 155                 160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
                165                 170                 175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
            180                 185                 190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
        195                 200                 205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
    210                 215                 220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225                 230                 235                 240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
                245                 250                 255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
            260                 265                 270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
        275                 280                 285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
    290                 295                 300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305                 310                 315                 320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
                325                 330                 335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
            340                 345                 350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
        355                 360                 365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
    370                 375                 380
Ser Thr Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val
385                 390                 395                 400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
                405                 410                 415
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420                 425                 430
```

<210> 86
<211> 432
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 86

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His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1               5                  10                  15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
            20                  25                  30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
        35                  40                  45

Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
    50                  55                  60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
65                  70                  75                  80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
                85                  90                  95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
            100                 105                 110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
        115                 120                 125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
    130                 135                 140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145                 150                 155                 160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
                165                 170                 175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
            180                 185                 190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
        195                 200                 205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
    210                 215                 220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225                 230                 235                 240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
                245                 250                 255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
            260                 265                 270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
        275                 280                 285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
    290                 295                 300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305                 310                 315                 320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
                325                 330                 335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
            340                 345                 350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
        355                 360                 365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
    370                 375                 380
Ser Thr Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val
385                 390                 395                 400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
                405                 410                 415
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420                 425                 430
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<210> 87
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 87
His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
1 5 10 15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
20 25 30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
35 40 45
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
50 55 60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
65 70 75 80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
85 90 95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
100 105 110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
115 120 125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
130 135 140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145 150 155 160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
165 170 175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
180 185 190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
195 200 205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
210 215 220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225 230 235 240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
245 250 255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
260 265 270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
275 280 285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
290 295 300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305 310 315 320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
325 330 335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
340 345 350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
355 360 365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
370 375 380
Ser Thr Ala Leu Glu Ala Tyr Gly Arg Ser Leu Asn Pro Asn Arg Val
385 390 395 400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
405 410 415

Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
420 425 430

<210> 88
<211> 423
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 88
Arg Asp Ile Pro Val Asn Pro Ile Cys Ile Tyr Arg Asn Pro Glu Lys
1 5 10 15
Lys Pro Gln Glu Arg Arg Gly Ala Gly Ala Gly Glu Gly Gln Asp Pro
20 25 30
Gly Val His Lys Pro Pro Val Trp Glu Leu Ser Arg Ala Asn Ser Arg
35 40 45
Phe Ala Val Val Phe Tyr Lys His Leu Ala Asp Ser Lys Asp Asn Glu
50 55 60
Glu Asn Ile Phe Leu Ser Pro Leu Ser Ile Ser Thr Ala Phe Ala Met
65 70 75 80
Thr Lys Leu Gly Ala Cys Gly Asp Thr Leu Gln Gln Leu Met Glu Val
85 90 95
Phe Gln Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Val His Phe
100 105 110
Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Lys Lys Ala Asn Lys Ser
115 120 125
Ser Glu Leu Ile Ser Ala Asn Arg Leu Phe Gly Glu Lys Ser Leu Val
130 135 140
Phe Asn Glu Thr Tyr Gln Asn Ile Ser Glu Ile Val Tyr Gly Ala Lys
145 150 155 160
Leu Trp Pro Leu Asn Phe Lys Glu Lys Pro Glu Leu Ser Arg Lys Ile
165 170 175
Ile Asn Glu Trp Val Ala Asn Lys Thr Glu Arg Arg Ile Thr Glu Val
180 185 190
Ile Pro Glu Lys Gly Ile Asp Asp Leu Thr Val Leu Val Leu Val Asn
195 200 205
Thr Ile Tyr Phe Lys Gly His Trp Lys Ser Gln Phe Pro Ala Pro Asn
210 215 220
Thr Arg Leu Asp Leu Phe His Lys Ala Asn Gly Glu Thr Cys Asn Val
225 230 235 240
Pro Ile Met Tyr Gln Glu Ser Arg Phe Pro Tyr Ala Phe Ile Gln Glu
245 250 255
Asp Lys Val Gln Val Leu Glu Leu Pro Tyr Lys Gly Asp Asp Ile Thr
260 265 270
Met Val Leu Val Leu Pro Lys Ala Gly Thr Pro Leu Val Glu Val Glu
275 280 285
Arg Asp Leu Thr Ser Asp Lys Leu Gln Asp Trp Ile Asp Ser Met Met
290 295 300
Glu Val Ser Leu Thr Val Ser Phe Pro Arg Phe Arg Val Glu Asp Ser
305 310 315 320
Phe Ser Val Lys Glu Lys Leu Arg Lys Met Gly Leu Glu Asp Leu Phe
325 330 335
Ser Pro Glu Asn Ala Lys Leu Pro Gly Ile Val Ala Gly Asp Arg Thr
340 345 350
Asp Leu Tyr Val Ser Glu Ala Phe His Lys Ala Phe Leu Glu Val Asn
355 360 365
Glu Glu Gly Ser Glu Ala Ser Ala Ala Thr Ala Val Val Ile Ser Gly
370 375 380
Arg Ser Phe Pro Met Asn Arg Ile Ile Phe Glu Ala Asn Arg Pro Phe

385 390 395 400
Leu Leu Phe Ile Arg Glu Ala Thr Leu Asn Thr Ile Ile Phe Met Gly
405 410 415
Arg Ile Ser Asp Pro Cys Ser
420

<210> 89
<211> 456

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 89
Met Tyr Leu Leu Ser Leu Leu Leu Leu Ser Leu Leu Gly Ser Ala Tyr
1 5 10 15
Leu Gln Pro Gln His Ala Asp Ile Cys Leu Ala Lys Pro Lys Asp Ile
20 25 30
Pro Leu Thr Pro Met Cys Val Tyr Arg Lys Pro Leu Glu Val Val Glu
35 40 45
Thr Glu Glu Lys Glu Lys Glu Pro Thr Thr Gln Glu Gln Lys Val Pro
50 55 60
Glu Ser Thr Asn Pro Arg Val Tyr Glu Leu Ser Gln Ala Asn Ala Lys
65 70 75 80
Phe Ala Ile Ala Phe Tyr Lys Asn Leu Ala Asp Ser Lys Arg Asp Lys
85 90 95
Glu Asn Ile Phe Met Ser Pro Leu Ser Ile Ser Gln Ala Phe Thr Met
100 105 110
Ala Lys Leu Gly Ala Cys Asn Asn Thr Leu Lys Gln Leu Met Glu Val
115 120 125
Phe His Phe Asp Thr Val Ser Glu Arg Ala Ser Asp Gln Ile His Tyr
130 135 140
Phe Phe Ala Lys Leu Asn Cys Arg Leu Phe Arg Lys Ala Asn Lys Ser
145 150 155 160
Ser Glu Leu Val Ser Val Asn Arg Leu Phe Gly Glu Lys Ser Leu Thr
165 170 175
Phe Asn Glu Thr Tyr Gln Asp Ile Ser Glu Ile Val Tyr Gly Ala Lys
180 185 190
Leu Trp Pro Leu Asn Phe Arg Asp Lys Pro Glu Leu Ser Arg Glu Ile
195 200 205
Ile Asn Asn Trp Val Ser Asn Lys Thr Glu Lys Arg Ile Thr Asp Val
210 215 220
Ile Pro Lys Asp Ala Ile Thr Pro Asp Thr Val Leu Val Leu Ile Asn
225 230 235 240
Ala Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Asn Ser Glu Asn
245 250 255
Thr Lys Met Asp Gln Phe His Pro Ala Lys Asn Ser Asn Cys Leu Thr
260 265 270
Ala Thr Met Tyr Gln Glu Gly Thr Phe Arg Tyr Gly Ser Phe Lys Asp
275 280 285
Asp Gly Val Gln Val Leu Glu Leu Pro Tyr Lys Gly Asp Asp Ile Thr
290 295 300
Met Val Leu Val Leu Pro Ser Gln Glu Thr Pro Leu Thr Thr Val Glu
305 310 315 320
Gln Asn Leu Thr Leu Glu Lys Leu Gly Asn Trp Leu Gln Lys Ser Arg
325 330 335
Glu Leu Gln Leu Ser Val Tyr Leu Pro Arg Phe Arg Val Glu Asp Ser
340 345 350
Phe Ser Val Lys Glu Lys Leu Gln Glu Met Gly Leu Val Asp Leu Phe
355 360 365

```
Asp Pro Asn Ser Ala Lys Leu Pro Gly Ile Ile Ala Gly Gly Arg Thr
    370                 375                 380
Asp Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn
385                 390                 395                 400
Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Ile Leu Thr Gly
                405                 410                 415

Arg Ser Leu Asn Leu Asn Arg Ile Ile Phe Arg Ala Asn Arg Pro Phe
            420                 425                 430
Leu Val Phe Ile Arg Glu Val Ala Ile Asn Ala Ile Leu Phe Met Gly
        435                 440                 445
Arg Val Ala Asn Pro Cys Thr Glu
    450                 455

<210> 90
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 90
Met Tyr Ser Pro Gly Ala Gly Ser Gly Ala Ala Gly Glu Arg Lys Leu
 1               5                  10                  15
Cys Leu Leu Ser Leu Leu Leu Ile Gly Ala Leu Gly Cys Ala Ile Cys
            20                  25                  30
His Gly Asn Pro Val Asp Asp Ile Cys Ile Ala Lys Pro Arg Asp Ile
        35                  40                  45
Pro Val Asn Pro Leu Cys Ile Tyr Arg Ser Pro Gly Lys Lys Ala Thr
    50                  55                  60
Glu Glu Asp Gly Ser Glu Gln Lys Val Pro Glu Ala Thr Asn Arg Arg
65                  70                  75                  80
Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Asn Phe Tyr
                85                  90                  95
Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser
            100                 105                 110
Pro Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys
        115                 120                 125
Asn Asp Thr Leu Lys Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile
    130                 135                 140
Ser Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn
145                 150                 155                 160
Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Asp Leu Val Ser Ala
                165                 170                 175
Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Ser Tyr Gln
            180                 185                 190
Asp Val Ser Glu Val Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe
        195                 200                 205
Lys Glu Asn Pro Glu Gln Ser Arg Val Thr Ile Asn Asn Trp Val Ala
    210                 215                 220
Asn Lys Thr Glu Gly Arg Ile Lys Asp Val Ile Pro Gln Gly Ala Ile
225                 230                 235                 240
Asn Glu Leu Thr Ala Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly
                245                 250                 255
Leu Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Pro Phe
            260                 265                 270
Tyr Lys Val Asp Gly Gln Ser Cys Pro Val Pro Met Met Tyr Gln Glu
        275                 280                 285
Gly Lys Phe Lys Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu
    290                 295                 300
Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys
```

305 310 315 320
Pro Glu Lys Ser Leu Ala Lys Val Glu Gln Glu Leu Thr Pro Glu Leu
325 330 335
Leu Gln Glu Trp Leu Asp Glu Leu Ser Glu Thr Met Leu Val Val His
340 345 350
Met Pro Arg Phe Arg Thr Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu
355 360 365
Gln Asp Met Gly Leu Ile Asp Leu Phe Ser Pro Glu Lys Ser Gln Leu
370 375 380
Pro Gly Ile Val Ala Gly Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala
385 390 395 400
Phe His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala
405 410 415
Ala Ser Thr Ser Val Val Ile Thr Gly Arg Ser Leu Asn Pro Asn Arg
420 425 430
Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Leu Ile Arg Glu Val
435 440 445
Ala Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val
450 455 460
Asn
465

<210> 91
<211> 1599
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 91
caccagcatc atctcctcca attcatccag ctactctgcc catgaagata atagttttca 60
ggcggattgc ctcagatcac actatctcca cttgcccagc cctgtggaag attagcggcc 120
atgtattcca atgtgatagg aactgtaacc tctggaaaaa ggaaggttta tcttttgtcc 180
ttgctgctca ttggcttctg ggactgcgtg acctgtcacg ggagccctgt ggacatctgc 240
acagccaagc cgcgggacat tcccatgaat cccatgtgca tttaccgctc cccggagaag 300
aaggcaactg aggatgaggg ctcagaacag aagatcccgg aggccaccaa ccggcgtgtc 360
tgggaactgt ccaaggccaa ttcccgcttt gctaccactt tctatcagca cctggcagat 420
tccaagaatg acaatgataa cattttcctg tcacccctga gtatctccac ggcttttgct 480
atgaccaagc tgggtgcctg taatgacacc ctccagcaac tgatggaggt atttaagttt 540
gacaccatat ctgagaaaac atctgatcag atccacttct tctttgccaa actgaactgc 600
cgactctatc gaaaagccaa caaatcctcc aagttagtat cagccaatcg ccttttgga 660
gacaaatccc ttaccttcaa tgagacctac caggacatca gtgagttggt atatggagcc 720
aagctccagc ccctggactt caaggaaaat gcagagcaat ccagagcggc catcaacaaa 780
tgggtgtcca ataagaccga aggccgaatc accgatgtca ttccctcgga agccatcaat 840
gagctcactg ttctggtgct ggttaacacc atttacttca agggcctgtg gaagtcaaag 900
ttcagccctg agaacacaag gaaggaactg ttctacaagg ctgatggaga gtcgtgttca 960
gcatctatga tgtaccagga aggcaagttc cgttatcggc gcgtggctga aggcacccag 1020
gtgcttgagt tgcccttcaa aggtgatgac atcaccatgg tcctcatctt gcccaagcct 1080
gagaagagcc tggccaaggt ggagaaggaa ctcaccccag aggtgctgca ggagtggctg 1140
gatgaattgg aggagatgat gctggtggtt cacatgcccc gcttccgcat tgaggacggc 1200
ttcagtttga aggagcagct gcaagacatg ggccttgtcg atctgttcag ccctgaaaag 1260
tccaaactcc caggtattgt tgcagaaggc cgagatgacc tctatgtctc agatgcattc 1320
cataaggcat ttcttgaggt aaatgaagaa ggcagtgaag cagctgcaag taccgctgtt 1380
gtgattgctg gccgttcgct aaaccccaac agggtgactt tcaaggccaa caggcccttc 1440
ctggttttta taagagaagt tcctctgaac actattatct tcatgggcag agtagccaac 1500
ccttgtgtta agtaaaatgt tcttattctt tgcacctctt cctatttttg gtttgtgaac 1560
agaagtaaaa ataaatacaa actacttcca tctcacatt 1599

<210> 92
<211> 430
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<221> VARIANT
<222> (386)...(389)
<223> Xaa = any amino acid

<400> 92

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Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
 1               5                  10                  15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
            20                  25                  30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
        35                  40                  45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
    50                  55                  60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65                  70                  75                  80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
                85                  90                  95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
            100                 105                 110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
        115                 120                 125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
    130                 135                 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145                 150                 155                 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
                165                 170                 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
            180                 185                 190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
        195                 200                 205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
    210                 215                 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                 230                 235                 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                245                 250                 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
            260                 265                 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
        275                 280                 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
    290                 295                 300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                 310                 315                 320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325                 330                 335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
            340                 345                 350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
        355                 360                 365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
    370                 375                 380
Ala Xaa Xaa Xaa Xaa Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                 390                 395                 400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                405                 410                 415
```

Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
420 425 430

<210> 93
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 93
Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1 5 10 15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
20 25 30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35 40 45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50 55 60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65 70 75 80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
85 90 95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
100 105 110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
115 120 125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
130 135 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145 150 155 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
165 170 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
180 185 190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
195 200 205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
210 215 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225 230 235 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
245 250 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
260 265 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
275 280 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
290 295 300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305 310 315 320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
325 330 335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
340 345 350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
355 360 365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
370 375 380
Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe

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385                 390                 395                 400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                405                 410                 415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420                 425                 430
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